

SEQUENCE LISTING

<110> FEDER, J.N.
MINTIER, G.
RAMANATHAN, C.S.
HAWKEN, D.R.
CACACE, A.
BARBER, L.
KORNACKER, M.G.

<120> A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY4,
EXPRESSED HIGHLY IN PROSTATE, COLON, AND LUNG

<130> D0039NP/3053-4117US3

<140> TBA

<141> 2001-09-26

<150> 60/235,833

<151> 2000-09-27

<150> 60/261,776

<151> 2001-01-16

<150> 60/305,351

<151> 2001-07-13

<150> 60/313,202

<151> 2001-08-17

<160> 60

<170> PatentIn Ver. 2.1

<210> 1

<211> 957

<212> DNA

<213> Homo sapiens

<400> 1

```
atgatggtgg atcccaatgg caatgaatcc agtgctacat acttcacccct aataggcctc 60
cctgggtttag aagaggetca gttctgggtg gccttcccat tgtgctccct ctaccttatt 120
gctgtgctag gtaacttgac aatcatctac attgtgcgga ctgagcacag cctgcatgag 180
cccattgtata tatttctttg catgctttca ggcattgaca tcctcatctc cacctcatcc 240
atgccccaaa tgctggccat cttctgggtc aattccacta ccatccagtt tgatgcttgt 300
ctgctacaga tgtttgccat ccactcctta tctggcatgg aatccacagt gctgctggcc 360
atggcttttg accgctatgt ggccatctgt caccactgc gccatgccac agtacttacg 420
ttgcctcgtg tcacaaaaat tggtgtggct gctgtggtgc ggggggctgc actgatggca 480
```

ccccttcctg tcttcatcaa gcagctgccc ttctgccgct ccaatatcct ttcccattcc 540
 tactgcctac accaagatgt catgaagctg gcctgtgatg atatccgggt caatgtcgtc 600
 tatggcetta tegtcatcat ctccgccatt ggcttgact cacttctcat ctcttctca 660
 tatctgctta ttcttaagac tgtgttgaggc ttgacacgtg aagcccaggc caaggcattt 720
 ggcacttgcg tctctcatgt gtgtgctgtg ttcatatctt atgtaccttt cattggattg 780
 tccatgggtgc atcgcttttag caagcggcgt gactctccgc tgcccgtcat cttggccaat 840
 atctatctgc tggttcctcc tgtgctcaac ccaattgtct atggagtga gacaaaggag 900
 attcgacagc gcacccctcg acttttccat gtggccacac acgcttcaga gccctag 957

<210> 2

<211> 318

<212> PRT

<213> Homo sapiens

<400> 2

Met Met Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr Phe Ile
 1 5 10 15
 Leu Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln Phe Trp Leu Ala Phe
 20 25 30
 Pro Leu Cys Ser Leu Tyr Leu Ile Ala Val Leu Gly Asn Leu Thr Ile
 35 40 45
 Ile Tyr Ile Val Arg Thr Glu His Ser Leu His Glu Pro Met Tyr Ile
 50 55 60
 Phe Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr Ser Ser
 65 70 75 80
 Met Pro Lys Met Leu Ala Ile Phe Trp Phe Asn Ser Thr Thr Ile Gln
 85 90 95
 Phe Asp Ala Cys Leu Leu Gln Met Phe Ala Ile His Ser Leu Ser Gly
 100 105 110
 Met Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala
 115 120 125
 Ile Cys His Pro Leu Arg His Ala Thr Val Leu Thr Leu Pro Arg Val
 130 135 140
 Thr Lys Ile Gly Val Ala Ala Val Val Arg Gly Ala Ala Leu Met Ala
 145 150 155 160
 Pro Leu Pro Val Phe Ile Lys Gln Leu Pro Phe Cys Arg Ser Asn Ile
 165 170 175

Leu Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys
 180 185 190

Asp Asp Ile Arg Val Asn Val Val Tyr Gly Leu Ile Val Ile Ile Ser
 195 200 205

Ala Ile Gly Leu Asp Ser Leu Leu Ile Ser Phe Ser Tyr Leu Leu Ile
 210 215 220

Leu Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys Ala Phe
 225 230 235 240

Gly Thr Cys Val Ser His Val Cys Ala Val Phe Ile Phe Tyr Val Pro
 245 250 255

Phe Ile Gly Leu Ser Met Val His Arg Phe Ser Lys Arg Arg Asp Ser
 260 265 270

Pro Leu Pro Val Ile Leu Ala Asn Ile Tyr Leu Leu Val Pro Pro Val
 275 280 285

Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Glu Ile Arg Gln Arg
 290 295 300

Ile Leu Arg Leu Phe His Val Ala Thr His Ala Ser Glu Pro
 305 310 315

<210> 3
 <211> 1381
 <212> DNA
 <213> Homo sapiens

<400> 3
 ccacgcgtcc gctctgccct gaatccagga tagaccagga caacaagatg agtggctaac 60
 tgtaggatgg tgtccatctg tgctctaggg gaggagtagc atcaaaggag aagcaagaac 120
 tgagaactgt ttggggcact gaagaagtag gactaaggaa gagttagggg gttagtacaa 180
 atctgaggcc tggttttctg gaaagagacc agagactgac cttattgcat gtcatacaac 240
 atgcttgctt agagaccctt aattttatttt cttctcttac tctttctgag gaagcatgag 300
 ccacaccctc agttagtttt gtataatctt aggccttgatg agaataaat cttagtcttg 360
 aaggcttttaa aggggaagaa atagctgtct gtgttagtgg tgtgtcagtc agcaggagaa 420
 cctgctaggg gtggaaggag gagggtagga gtatagccta gaccatgagt agataccccg 480
 ctccaccttg aaagtctcct actggacctc ttatgatgga gttaatacct cctgtttcct 540
 ctattccaga ttgttttcag tttccagaag gcaaaaactga catctcccag gagtccaagt 600
 aggagattag ggccctcccg ccctatctac tcagtgtctag ccttgggctaa gagagaggaa 660
 attcctgcct agaggggaaa atctgcagga cttcgttacc actttcactt tggcagagga 720
 aggaggtcag ggatggaagg ggaagtgagt ctagaaatta aaacatagaa ttctgtctac 780

aggtggtgga gagcctttct gaaagtgtt ctgggttgag gctgtcacct agattttata 840
 ttagagttta agtgttccaa aaaattaaga agcaggaagt agaaaagaga acaatttcag 900
 aagcagacga aaggaacagt aataggaaga tctagcaagg atgtggtggg gcagtttcag 960
 tgtgagatgc catggacagg aaaatggcag catatgtgtg tgtgtgtgtg tgtgtgtgtg 1020
 tccatgagac agagagacat aaataactaa ataaaaaggc atatcacaaa gaggggctcc 1080
 tgcttcagct tgagtcctgg atgcaaagac atgtggactg ggatcctagc aacctatctg 1140
 cagccaagga catgacgtta gacgccccaa gaaaaggaaa attggtcaaa cataggaaga 1200
 gcactcaagt gccagctaca gtgaatgaca aatacccacc acaagcacia gctctacatt 1260
 cacaaaaact tggaaaacac aagttcatag actgggcaac cctgagtagt ggagagatca 1320
 ccagccatgt ttcaggttgt accctctacc tgcctggtgc tggtcacagt tcagcttctt 1380
 c 1381

<210> 4

<211> 2034

<212> DNA

<213> Homo sapiens

<400> 4

gtgtcagtga tcaaacttct tttccattca gagtcctctg attcagattt taatgttaac 60
 attttggaag acagtattca gaaaaaaaaat ttccttaata aaaatacaac tcagatcctt 120
 caaatatgaa actggttggg gaatctccat tttttcaata ttattttctt ctttgttttc 180
 ttgtacata taattattaa taccctgact aggttgtggg tggaggggta ttacttttca 240
 ttttaccatg cagtccaaat ctaaactgct tctactgatg gtttacagca ttctgagata 300
 agaatggtac atctagagaa catttgccaa aggcctaagc acggcaaagg aaaataaaca 360
 cagaatataa taaaatgaga taatctagct taaaactata acttcctctt cagaactccc 420
 aaccacattg gatctcagaa aaatactgtc ttcaaaatga cttctacaga gaagaaataa 480
 tttttcctct ggacactagc acttaagggg aagattggaa gtaaagcctt gaaaagagta 540
 catttaccta cgtaaatgaa agttgacaca ctgttctgag agttttcaca gcatatggac 600
 cctgtttttc ctatttaatt ttcttatcaa ccctttaatt aggcaaagat attattagta 660
 ccctcattgt agccatggga aaattgatgt tcagtgggga tcagtgaatt aaatgggggc 720
 atacaagtat aaaaattaaa aaaaaagac ttcattgcca atctcatatg atgtggaaga 780
 actgttagag agaccaacag ggtagtgggt tagagatttc cagagtctta cattttctag 840
 aggaggtatt taattttctc tcaactctct cagtgttgta ttaggaatt tcctggcaac 900
 agaactcatg gctttaatcc cactagctat tgcttattgt cctggtccaa ttgccaatta 960
 cctgtgtctt ggaagaagtg atttctaggt tcaccattat ggaagattct tattcagaaa 1020
 gtctgcatag ggcttatagc aagttattta tttttaaaag ttccataggt gattctgata 1080
 ggagtgagg ttagggagcc accagttatg atgggaagta tggaatggca ggtcttgaag 1140
 ataacattgg ccttttgagt gtgactcgta gctggaaagt gagggaatct tcaggaccat 1200
 gctttatttg gggctttgtg cagtatggaa cagggacttt gagaccagga aagcaatctg 1260
 acttaggcat gggaatcagg catttttgct tctgaggggc tattaccaag ggtaaatagg 1320
 tttcatcttc aacaggatat gacaacagtg ttaaccaaga aactcaaatt acaataacta 1380
 aaacatgtga tcatatatgt ggtaagtttc attttctttt tcaatcctca ggttcctga 1440
 tatggattcc tataacatgc tttcatcccc ttttgtaatg gatatcatat ttggaaatgc 1500
 ctatttaata cttgtatttg ctgctggact gtaagcccat gagggcactg tttattattg 1560
 aatgtcatct ctgttcatca ttgactgctc tttgctcatc attgaatccc ccagcaaagt 1620
 gcctagaaca taatagtgt tatgcttgac accggttatt tttcatcaaa cctgattcct 1680
 tctgtcctga acacatagcc aggcaatttt ccagccttct ttgagttggg tattattaaa 1740

ttctggccat tacttccaat gtgagtggaa gtgacatgtg caatttctat acctggctca 1800
 taaaaccctc ccatgtgcag cctttcatgt tgacattaaa tgtgacttgg gaagctatgt 1860
 gttacacaga gtaaatacacc agaagcctgg atttctgaaa aaactgtgca gagccaaacc 1920
 tctgtcattt gcaactccca cttgtatttg tacgaggcag ttggataagt gaaaaataaa 1980
 gtactattgt gtcaagtcaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 2034

<210> 5

<211> 80

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
 oligos

<400> 5

gatccacat catgaagaag ctgaactgtg accagcacca ggcaggtaga ggctcaaccg 60
 tatggaagga atgtgtgacc 80

<210> 6

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
 oligos

<400> 6

actgagcaca gcctgcatga 20

<210> 7

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
 oligos

<400> 7

tctgtagcag acaagcatca aactg 25

<210> 8

<211> 311
 <212> PRT
 <213> MOUSE

<400> 8

Met Trp Pro Asn Ser Ser Asp Ala Pro Phe Leu Leu Thr Gly Phe Leu
 1 5 10 15

Gly Leu Glu Met Ile His His Trp Ile Ser Ile Pro Phe Phe Val Ile
 20 25 30

Tyr Phe Ser Ile Ile Val Gly Asn Gly Thr Leu Leu Phe Ile Ile Trp
 35 40 45

Ser Asp His Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Ala Val Leu
 50 55 60

Ala Ser Met Asp Leu Gly Met Thr Leu Thr Thr Met Pro Thr Val Leu
 65 70 75 80

Gly Val Leu Val Leu Asn Gln Arg Glu Ile Val His Gly Ala Cys Phe
 85 90 95

Ile Gln Ser Tyr Phe Ile His Ser Leu Ala Ile Val Glu Ser Gly Val
 100 105 110

Leu Leu Ala Met Ser Tyr Asp Arg Phe Val Ala Ile Cys Thr Pro Leu
 115 120 125

His Tyr Asn Ser Ile Leu Thr Asn Ser Arg Val Met Lys Met Ala Leu
 130 135 140

Gly Ala Leu Leu Arg Gly Phe Val Ser Ile Val Pro Pro Ile Met Pro
 145 150 155 160

Leu Phe Trp Phe Pro Tyr Cys His Ser His Val Leu Ser His Ala Phe
 165 170 175

Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Ala Asp Ile Thr Phe
 180 185 190

Asn Leu Ile Tyr Pro Val Val Leu Val Ala Leu Thr Phe Phe Leu Asp
 195 200 205

Ala Leu Ile Ile Ile Phe Ser Tyr Val Leu Ile Leu Lys Lys Val Met
 210 215 220

Gly Ile Ala Ser Gly Glu Glu Arg Lys Lys Ser Leu Asn Thr Cys Val

09966459 092604

225 230 235 240
 Ser His Ile Ser Cys Val Leu Val Phe Tyr Ile Thr Val Ile Gly Leu
 245 250 255
 Thr Phe Ile His Arg Phe Gly Lys Asn Ala Pro His Val Val His Ile
 260 265 270
 Thr Met Ser Tyr Val Tyr Phe Leu Phe Pro Pro Phe Met Asn Pro Ile
 275 280 285
 Ile Tyr Ser Ile Lys Thr Lys Gln Ile Gln Arg Ser Ile Leu Arg Leu
 290 295 300
 Leu Ser Lys His Ser Arg Thr
 305 310

 <210> 9
 <211> 307
 <212> PRT
 <213> MOUSE

 <400> 9
 Met Trp Ser Asn Ile Ser Ala Ala Pro Phe Leu Leu Thr Gly Phe Pro
 1 5 10 15
 Gly Leu Glu Ala Ala His His Trp Ile Ser Ile Pro Phe Phe Ala Ile
 20 25 30
 Tyr Ile Ser Val Leu Leu Gly Asn Gly Thr Leu Leu Tyr Leu Ile Lys
 35 40 45
 Asp Asp His Asn Leu His Glu Pro Met Tyr Tyr Phe Leu Ala Met Leu
 50 55 60
 Ala Gly Thr Asp Leu Thr Val Thr Leu Thr Thr Met Pro Thr Val Met
 65 70 75 80
 Ala Val Leu Trp Val Asn His Arg Glu Ile Arg His Gly Ala Cys Phe
 85 90 95
 Leu Gln Ala Tyr Ile Ile His Ser Leu Ser Ile Val Glu Ser Gly Val
 100 105 110
 Leu Leu Ala Met Ser Tyr Asp Arg Phe Val Ala Ile Cys Thr Pro Leu
 115 120 125

09966459 092601

His Tyr Asn Ser Ile Leu Thr Asn Ser Arg Val Ile Ala Ile Gly Leu
130 135 140

Gly Val Val Leu Arg Gly Phe Leu Ser Leu Val Pro Pro Ile Leu Pro
145 150 155 160

Leu Phe Trp Phe Ser Tyr Cys Arg Ser His Val Leu Ser His Ala Phe
165 170 175

Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Ala Asp Ile Thr Phe
180 185 190

Asn Arg Ile Tyr Pro Val Val Leu Val Ala Leu Thr Phe Phe Leu Asp
195 200 205

Ala Leu Ile Ile Val Phe Ser Tyr Val Leu Ile Leu Lys Thr Val Met
210 215 220

Gly Ile Ala Ser Gly Glu Glu Arg Ala Lys Ala Leu Asn Thr Cys Val
225 230 235 240

Ser His Ile Ser Cys Val Leu Val Phe Tyr Ile Thr Val Ile Gly Leu
245 250 255

Thr Phe Ile His Arg Phe Gly Lys Asn Ala Pro His Val Val His Ile
260 265 270

Thr Met Ser Tyr Val Tyr Phe Leu Phe Pro Pro Phe Met Asn Pro Ile
275 280 285

Ile Tyr Ser Ile Lys Thr Lys Gln Ile Gln Arg Ser Val Leu His Leu
290 295 300

Leu Ser Val
305

<210> 10
<211> 312
<212> PRT
<213> HUMAN

<400> 10
Met Trp Pro Asn Ile Thr Ala Ala Pro Phe Leu Leu Thr Gly Phe Pro
1 5 10 15

Gly Leu Glu Ala Ala His His Trp Ile Ser Ile Pro Phe Phe Ala Val
20 25 30

Tyr Val Cys Ile Leu Leu Gly Asn Gly Met Leu Leu Tyr Leu Ile Lys
 35 40 45
 His Asp His Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Thr Met Leu
 50 55 60
 Ala Gly Thr Asp Leu Met Val Thr Leu Thr Thr Met Pro Thr Val Met
 65 70 75 80
 Gly Ile Leu Trp Val Asn His Arg Glu Ile Ser Ser Val Gly Cys Phe
 85 90 95
 Leu Gln Ala Tyr Phe Ile His Ser Leu Ser Val Val Glu Ser Gly Ser
 100 105 110
 Leu Leu Ala Met Ala Tyr Asp Arg Phe Ile Ala Ile Arg Asn Pro Leu
 115 120 125
 Arg Tyr Ala Ser Ile Phe Thr Asn Thr Arg Val Ile Ala Leu Gly Val
 130 135 140
 Gly Val Phe Leu Arg Gly Phe Val Ser Ile Leu Pro Val Ile Leu Arg
 145 150 155 160
 Leu Phe Ser Phe Ser Tyr Cys Lys Ser His Val Ile Thr Arg Ala Phe
 165 170 175
 Cys Leu His Gln Glu Ile Met Arg Leu Ala Cys Ala Asp Ile Thr Phe
 180 185 190
 Asn Arg Leu Tyr Pro Val Ile Leu Ile Ser Leu Thr Ile Phe Leu Asp
 195 200 205
 Ser Leu Ile Ile Leu Phe Ser Tyr Ile Leu Ile Leu Asn Thr Val Ile
 210 215 220
 Gly Ile Ala Ser Gly Glu Glu Gln Thr Lys Ala Leu Asn Thr Cys Val
 225 230 235 240
 Ser His Phe Cys Ala Val Leu Ile Phe Tyr Ile Pro Leu Ala Gly Leu
 245 250 255
 Ser Ile Ile His Arg Tyr Gly Arg Asn Ala Pro Pro Ile Ser His Ala
 260 265 270
 Val Met Ala Asn Val Tyr Leu Phe Val Pro Pro Ile Leu Asn Pro Val
 275 280 285

0956459.092601

Ile Tyr Ser Ile Lys Thr Lys Gln Ile Gln Tyr Gly Ile Ile Arg Leu
 290 295 300

Leu Ser Lys His Arg Phe Ser Arg
 305 310

<210> 11
 <211> 319
 <212> PRT
 <213> CHICKEN

<400> 11
 Met Tyr Pro Arg Asn Ser Ser Gln Ala Gln Pro Phe Leu Leu Ala Gly
 1 5 10 15

Leu Pro Gly Met Ala Gln Phe His His Trp Val Phe Leu Pro Phe Gly
 20 25 30

Leu Met Tyr Leu Val Ala Val Leu Gly Asn Gly Thr Ile Leu Leu Val
 35 40 45

Val Arg Val His Arg Gln Leu His Gln Pro Met Tyr Tyr Phe Leu Leu
 50 55 60

Met Leu Ala Thr Thr Asp Leu Gly Leu Thr Leu Ser Thr Leu Pro Thr
 65 70 75 80

Val Leu Arg Val Phe Trp Leu Gly Ala Met Glu Ile Ser Phe Pro Ala
 85 90 95

Cys Leu Ile Gln Met Phe Cys Ile His Val Phe Ser Phe Met Glu Ser
 100 105 110

Ser Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Cys
 115 120 125

Pro Leu Arg Tyr Ser Ser Ile Leu Thr Gly Ala Arg Val Ala Gln Ile
 130 135 140

Gly Leu Gly Ile Ile Cys Arg Cys Thr Leu Ser Leu Leu Pro Leu Ile
 145 150 155 160

Cys Leu Leu Thr Trp Leu Pro Phe Cys Arg Ser His Val Leu Ser His
 165 170 175

Pro Tyr Cys Leu His Gln Asp Ile Ile Arg Leu Ala Cys Thr Asp Ala

00966459 092601

180 185 190
Thr Leu Asn Ser Leu Tyr Gly Leu Ile Leu Val Leu Val Ala Ile Leu
195 200 205
Asp Phe Val Leu Ile Ala Leu Ser Tyr Ile Met Ile Phe Arg Thr Val
210 215 220
Leu Gly Ile Thr Ser Lys Glu Glu Gln Thr Lys Ala Leu Asn Thr Cys
225 230 235 240
Val Ser His Phe Cys Ala Val Leu Ile Phe Tyr Ile Pro Leu Ala Gly
245 250 255
Leu Ser Ile Ile His Arg Tyr Gly Arg Asn Ala Pro Pro Ile Ser His
260 265 270
Ala Val Met Ala Asn Val Tyr Leu Phe Val Pro Pro Ile Leu Asn Pro
275 280 285
Val Leu Tyr Ser Met Lys Ser Lys Ala Ile Cys Lys Gly Leu Leu Arg
290 295 300
Leu Leu Cys Gln Arg Ala Ala Trp Pro Gly His Ala Gln Asn Cys
305 310 315
<210> 12
<211> 320
<212> PRT
<213> RAT

<400> 12
Met Ser Ser Cys Asn Phe Thr His Ala Thr Phe Met Leu Ile Gly Ile
1 5 10 15
Pro Gly Leu Glu Glu Ala His Phe Trp Phe Gly Phe Pro Leu Leu Ser
20 25 30
Met Tyr Ala Val Ala Leu Phe Gly Asn Cys Ile Val Val Phe Ile Val
35 40 45
Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met
50 55 60
Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile
65 70 75 80

Leu Ala Leu Phe Trp Phe Asp Ser Arg Glu Ile Thr Phe Asp Ala Cys
 85 90 95

Leu Ala Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr
 100 105 110

Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro
 115 120 125

Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Val Gln Ile Gly
 130 135 140

Met Val Ala Leu Val Arg Gly Ser Leu Phe Phe Phe Pro Leu Pro Leu
 145 150 155 160

Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser
 165 170 175

Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Thr Asp Thr Leu
 180 185 190

Pro Asn Val Val Tyr Gly Leu Thr Ala Ile Leu Leu Val Met Gly Val
 195 200 205

Asp Val Met Phe Ile Ser Leu Ser Tyr Phe Leu Ile Ile Arg Ala Val
 210 215 220

Leu Gln Leu Pro Ser Lys Ser Glu Arg Ala Lys Ala Phe Gly Thr Cys
 225 230 235 240

Val Ser His Ile Gly Val Val Leu Ala Phe Tyr Val Pro Leu Ile Gly
 245 250 255

Leu Ser Val Val His Arg Phe Gly Asn Ser Leu Asp Pro Ile Val His
 260 265 270

Val Leu Met Gly Asp Val Tyr Leu Leu Leu Pro Pro Val Ile Asn Pro
 275 280 285

Ile Ile Tyr Gly Ala Lys Thr Lys Gln Ile Arg Thr Arg Val Leu Ala
 290 295 300

Met Phe Lys Ile Ser Cys Asp Lys Asp Ile Glu Ala Gly Gly Asn Thr
 305 310 315 320

0906459 092601

<210> 13
 <211> 321
 <212> PRT
 <213> MOUSE

<400> 13

Met Asn Ser Lys Ala Ser Met Leu Gly Thr Asn Phe Thr Ile Ile His
 1 5 10 15

Pro Thr Val Phe Ile Leu Leu Gly Ile Pro Gly Leu Glu Gln Tyr His
 20 25 30

Thr Trp Leu Ser Ile Pro Phe Cys Leu Met Tyr Ile Ala Ala Val Leu
 35 40 45

Gly Asn Gly Ala Leu Ile Leu Val Val Leu Ser Glu Arg Thr Leu His
 50 55 60

Glu Pro Met Tyr Val Phe Leu Ser Met Leu Ala Gly Thr Asp Ile Leu
 65 70 75 80

Leu Ser Thr Thr Thr Val Pro Lys Thr Leu Ala Ile Phe Trp Phe His
 85 90 95

Ala Gly Glu Ile Pro Phe Asp Ala Cys Ile Ala Gln Met Phe Phe Ile
 100 105 110

His Val Ala Phe Val Ala Glu Ser Gly Ile Leu Leu Ala Met Ala Phe
 115 120 125

Asp Arg Tyr Val Ala Ile Cys Thr Pro Leu Arg Tyr Ser Ala Val Leu
 130 135 140

Thr Pro Met Ala Ile Gly Lys Met Thr Leu Ala Ile Trp Gly Arg Ser
 145 150 155 160

Ile Gly Thr Ile Phe Pro Ile Ile Phe Leu Leu Lys Arg Leu Ser Tyr
 165 170 175

Cys Arg Thr Asn Val Ile Pro His Ser Tyr Cys Glu His Ile Gly Val
 180 185 190

Ala Arg Leu Ala Cys Ala Asp Ile Thr Val Asn Ile Trp Tyr Gly Phe
 195 200 205

Ser Val Pro Met Ala Ser Val Leu Val Asp Val Ala Leu Ile Gly Ile
 210 215 220

00966459-092601

Ser Tyr Thr Leu Ile Leu Gln Ala Val Phe Arg Leu Pro Ser Gln Asp
225 230 235 240

Ala Arg His Lys Ala Leu Asn Thr Cys Gly Ser His Ile Gly Val Ile
245 250 255

Leu Leu Phe Phe Ile Pro Ser Phe Phe Thr Phe Leu Thr His Arg Phe
260 265 270

Gly Lys Asn Ile Pro His His Val His Ile Leu Leu Ala Asn Leu Tyr
275 280 285

Val Leu Val Pro Pro Met Leu Asn Pro Ile Ile Tyr Gly Ala Lys Thr
290 295 300

Lys Gln Ile Arg Asp Ser Met Thr Arg Met Leu Ser Val Val Trp Lys
305 310 315 320

Ser

<210> 14

<211> 326

<212> PRT

<213> MOUSE

<400> 14

Met Lys Val Ala Ser Ser Phe His Asn Asp Thr Asn Pro Gln Asp Val
1 5 10 15

Trp Tyr Val Leu Ile Gly Ile Pro Gly Leu Glu Asp Leu His Ser Trp
20 25 30

Ile Ala Ile Pro Ile Cys Ser Met Tyr Ile Val Ala Val Ile Gly Asn
35 40 45

Val Leu Leu Ile Phe Leu Ile Val Thr Glu Arg Ser Leu His Glu Pro
50 55 60

Met Tyr Phe Phe Leu Ser Met Leu Ala Leu Ala Asp Leu Leu Leu Ser
65 70 75 80

Thr Ala Thr Ala Pro Lys Met Leu Ala Ile Phe Trp Phe His Ser Arg
85 90 95

Gly Ile Ser Phe Gly Ser Cys Val Ser Gln Met Phe Phe Ile His Phe

0906459.092601

00966459-092601

100	105	110
Ile Phe Val Ala Glu Ser Ala	Ile Leu Leu Ala Met	Ala Phe Asp Arg
115	120	125
Tyr Val Ala Ile Cys Tyr Pro	Leu Arg Tyr Thr Thr	Ile Leu Thr Ser
130	135	140
Ser Val Ile Gly Lys Ile Gly Thr	Ala Ala Val Val Arg Ser Phe	Leu
145	150	155 160
Ile Cys Phe Pro Phe Ile Phe	Leu Val Tyr Arg Leu Leu Tyr	Cys Gly
165	170	175
Lys His Ile Ile Pro His Ser Tyr	Cys Glu His Met Gly Ile Ala	Arg
180	185	190
Leu Ala Cys Asp Asn Ile Thr Val	Asn Ile Ile Tyr Gly Leu Thr	Met
195	200	205
Ala Leu Leu Ser Thr Gly Leu Asp	Ile Leu Leu Ile Ile Ile Ser Tyr	
210	215	220
Thr Met Ile Leu Arg Thr Val Phe	Gln Ile Pro Ser Trp Ala Ala	Arg
225	230	235 240
Tyr Lys Ala Leu Asn Thr Cys Gly	Ser His Ile Cys Val Ile Leu Leu	
245	250	255
Phe Tyr Thr Pro Ala Phe Phe Ser	Phe Phe Ala His Arg Phe Gly Gly	
260	265	270
Lys Thr Val Pro Arg His Ile His	Ile Leu Val Ala Asn Leu Tyr Val	
275	280	285
Val Val Pro Pro Met Leu Asn Pro	Ile Ile Tyr Gly Val Lys Thr Lys	
290	295	300
Gln Ile Gln Asp Arg Val Val Phe	Leu Phe Ser Ser Val Ser Thr Cys	
305	310	315 320
Gln His Asp Ser Arg Cys		
325		

<210> 15
<211> 318
<212> PRT

<213> MOUSE

<400> 15

Met Ser Pro Gly Asn Ser Ser Trp Ile His Pro Ser Ser Phe Leu Leu
1 5 10 15

Leu Gly Ile Pro Gly Leu Glu Glu Leu Gln Phe Trp Leu Gly Leu Pro
20 25 30

Phe Gly Thr Val Tyr Leu Ile Ala Val Leu Gly Asn Val Ile Ile Leu
35 40 45

Phe Val Ile Tyr Leu Glu His Ser Leu His Gln Pro Met Phe Tyr Leu
50 55 60

Leu Ala Ile Leu Ala Val Thr Asp Leu Gly Leu Ser Thr Ala Thr Val
65 70 75 80

Pro Arg Ala Leu Gly Ile Phe Trp Phe Gly Phe His Lys Ile Ala Phe
85 90 95

Arg Asp Cys Val Ala Gln Met Phe Phe Ile His Leu Phe Thr Gly Ile
100 105 110

Glu Thr Phe Met Leu Val Ala Met Ala Phe Asp Arg Tyr Ile Ala Ile
115 120 125

Cys Asn Pro Leu Arg Tyr Asn Thr Ile Leu Thr Asn Arg Thr Ile Cys
130 135 140

Ile Ile Val Gly Val Gly Leu Phe Lys Asn Phe Ile Leu Val Phe Pro
145 150 155 160

Leu Ile Phe Leu Ile Leu Arg Leu Ser Phe Cys Gly His Asn Ile Ile
165 170 175

Pro His Thr Tyr Cys Glu His Met Gly Ile Ala Arg Leu Ala Cys Val
180 185 190

Ser Ile Lys Val Asn Val Leu Phe Gly Leu Ile Leu Ile Ser Met Ile
195 200 205

Leu Leu Asp Val Val Leu Ser Ala Leu Ser Tyr Ala Lys Ile Leu His
210 215 220

Ala Val Phe Lys Leu Pro Ser Trp Glu Ala Arg Leu Lys Ala Leu Asn
225 230 235 240

09066459-092601

Thr Cys Gly Ser His Val Cys Val Ile Leu Ala Phe Phe Thr Pro Ala
 245 250 255

Phe Phe Ser Phe Leu Thr His Arg Phe Gly His Asn Ile Pro Arg Tyr
 260 265 270

Ile His Ile Leu Leu Ala Asn Leu Tyr Val Ile Ile Pro Xaa Ala Leu
 275 280 285

Asn Pro Ile Ile Tyr Gly Val Arg Thr Lys Gln Ile Gln Asp Arg Ala
 290 295 300

Val Thr Ile Leu Cys Asn Glu Val Gly Gln Leu Ala Asp Asp
 305 310 315

<210> 16
 <211> 316
 <212> PRT
 <213> MOUSE

<400> 16
 Met Ile Lys Phe Asn Gly Ser Val Phe Met Pro Ser Val Leu Thr Leu
 1 5 10 15

Val Gly Ile Pro Gly Leu Glu Ser Val Gln Cys Trp Ile Gly Ile Pro
 20 25 30

Phe Cys Val Met Tyr Ile Ile Ala Met Ile Gly Asn Ser Leu Ile Leu
 35 40 45

Val Ile Ile Lys Ser Glu Lys Ser Leu His Ile Pro Met Tyr Ile Phe
 50 55 60

Leu Ala Ile Leu Ala Val Thr Asp Ile Ala Leu Ser Thr Cys Ile Leu
 65 70 75 80

Pro Lys Met Leu Gly Ile Phe Trp Phe His Met Pro Gln Ile Ser Phe
 85 90 95

Asp Ala Cys Leu Leu Gln Met Glu Leu Ile His Ser Phe Gln Ala Thr
 100 105 110

Glu Ser Gly Ile Leu Leu Ala Met Ala Leu Asp Arg Tyr Val Ala Ile
 115 120 125

Cys Asn Pro Leu Arg His Ala Thr Ile Phe Ser Pro Gln Leu Thr Thr
 130 135 140

0966459-092604

Cys Leu Gly Ala Gly Ala Leu Leu Arg Ser Leu Ile Thr Thr Phe Pro
145 150 155 160

Leu Ile Leu Leu Ile Lys Phe Cys Leu Lys Tyr Phe Arg Thr Thr Ile
165 170 175

Ile Ser His Ser Tyr Cys Glu His Met Ala Ile Val Lys Leu Ala Ala
180 185 190

Gln Asp Ile Arg Ile Asn Lys Ile Cys Gly Leu Leu Val Ala Phe Ala
195 200 205

Ile Leu Gly Phe Asp Ile Val Phe Ile Thr Phe Ser Tyr Val Arg Ile
210 215 220

Phe Ile Thr Val Phe Gln Leu Pro Gln Lys Glu Ala Arg Phe Lys Ala
225 230 235 240

Phe Asn Thr Cys Ile Ala His Ile Cys Val Phe Leu Gln Phe Tyr Leu
245 250 255

Leu Ala Phe Phe Ser Phe Phe Thr His Arg Phe Gly Ala His Ile Pro
260 265 270

Pro Tyr Val His Ile Leu Leu Ser Asp Leu Tyr Leu Leu Val Pro Pro
275 280 285

Phe Leu Asn Pro Ile Val Tyr Gly Ile Lys Thr Lys Gln Ile Arg Asp
290 295 300

Gln Val Leu Lys Met Phe Phe Ser Lys Lys Pro Leu
305 310 315

<210> 17

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
peptide

<400> 17

Met Met Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr Phe Ile
1 5 10 15

Leu Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln
20 25

<210> 18
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
peptide

<400> 18
Arg Thr Glu His Ser Leu His Glu Pro Met Tyr
1 5 10

<210> 19
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
peptide

<400> 19
Asn Ser Thr Thr Ile Gln Phe Asp Ala Cys Leu Leu Gln Met
1 5 10

<210> 20
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
peptide

<400> 20
His Pro Leu Arg His Ala Thr Val Leu Thr Leu Pro Arg Val Thr Lys
1 5 10 15

<210> 21
<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
peptide

<400> 21

Lys Gln Leu Pro Phe Cys Arg Ser Asn Ile Leu Ser His Ser Tyr Cys
1 5 10 15

Leu His Gln Asp Val Met Lys Leu Ala Cys Asp Asp Ile Arg
20 25 30

<210> 22

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
peptide

<400> 22

Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys Ala
1 5 10

<210> 23

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
peptide

<400> 23

His Arg Phe Ser Lys Arg Arg Asp Ser Pro
1 5 10

<210> 24

<211> 22

<212> PRT

<213> Artificial Sequence

0906459 092601

<220>

<223> Description of Artificial Sequence: Synthesized
peptide

<400> 24

Lys Thr Lys Glu Ile Arg Gln Arg Ile Leu Arg Leu Phe His Val Ala
1 5 10 15

Thr His Ala Ser Glu Pro
20

<210> 25

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Forward GPCR9
primer-

<400> 25

cctgtgctca acccaattgt ct

22

<210> 26

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Reverse GPCR9
primer-

<400> 26

actgacacct agggctctga ag

22

<210> 27

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: GAPDH-F3
forward primer

<400> 27

agccgagcca catcgct

17

<210> 28

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: GAPDH-R1
reverse primer

<400> 28

gtgaccaggc gcccaatac

19

<210> 29

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: GAPDH-PVIC
Taqman(R) Probe

<400> 29

caaatccgtt gactccgacc ttcacctt

28

<210> 30

<211> 39

<212> DNA

<213> Artificial Sequence

<400> 30

cccaagcttg caccatgatg gtggatccca atggcattg

39

<210> 31

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: HGPRBMY4 3'
primer

<400> 31

gaagatctct agggctctga agcgtgtgtg gcc

33

<210> 32

<211> 59

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: HGPRBMY4 3'
primer- Flag tag

<400> 32

gaagatctct acttgctgctc gtcgtccttg tagtccatgg gctctgaagc gtgtgtggc 59

<210> 33

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 33

Met Val His Arg Phe Ser Lys Arg Arg Asp Ser Pro Leu
1 5 10

<210> 34

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 34

Val Arg Thr Glu His Ser Leu His Glu Pro Met Tyr Ile Phe
1 5 10

<210> 35

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 35

Phe Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr
1 5 10

<210> 36

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 36

Ala Ile His Ser Leu Ser Gly Met Glu Ser Thr Val Leu Leu
1 5 10

<210> 37

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 37

His Arg Phe Ser Lys Arg Arg Asp Ser Pro Leu Pro Val Ile
1 5 10

<210> 38

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 38

T09260"65499660

Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr Phe Ile
1 5 10

<210> 39
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 39
Ile Ala Val Leu Gly Asn Leu Thr Ile Ile Tyr Ile Val Arg
1 5 10

<210> 40
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 40
Ala Ile Phe Trp Phe Asn Ser Thr Thr Ile Gln Phe Asp Ala
1 5 10

<210> 41
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 41
Met Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr Phe Ile Leu
1 5 10 15

<210> 42
<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 42

Leu Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln Phe Trp Leu Ala Phe
1 5 10 15

<210> 43

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 43

Ile His Ser Leu Ser Gly Met Glu Ser Thr Val Leu Leu Ala Met Ala
1 5 10 15

<210> 44

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 44

Gln Ala Lys Ala Phe Gly Thr Cys Val Ser His Val Cys Ala Val Phe
1 5 10 15

<210> 45

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

[illegible]

Asp Arg Tyr Val Ala Ile Cys His Pro Leu Arg
20 25

<220>
<223> Description of Artificial Sequence: Oligo 1;
N=A+G+C+T; K=C+G+T

```
<210> 47
<211> 95
<212> DNA
<213> Artificial Sequence
```

```
<400> 47
aaaaggaaaa aagcggccgc vnnvnnvnnv nnnvnnvnnv nvnvnnvnnv vnnvnnvnnv 60
nnvnnvnnvn nvnvnnvnnv qccqcccqqa cccqg                               95
```

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

1

5

<210> 49

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic 5'
Primer

<400> 49

gcagcagcgg ccgccagttc tggttggcct tcccattg

38

<210> 50

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic 3'
Primer

<400> 50

gcagcagtcg acgggctctg aagcgtgtgt ggccac

36

<210> 51

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic 5'
Primer

<400> 51

gcagcagcgg ccgcatgatg gtggatccca atggcaatg

39

<210> 52

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

09966459.092604

<223> Description of Artificial Sequence: Synthetic 3'
Primer

<400> 52

gcagcagtcg accttcactc catagacaat tggggttg

37

<210> 53

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 53

Gly Asp Phe Trp Tyr Glu Ala Cys Glu Ser Ser Cys Ala Phe Trp
1 5 10 15

<210> 54

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 54

Cys Leu Arg Ser Gly Thr Gly Cys Ala Phe Gln Leu Tyr Arg Phe
1 5 10 15

<210> 55

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 55

Phe Ala Gly Gln Ile Ile Trp Tyr Asp Ala Leu Asp Thr Leu Met
1 5 10 15

09965459 092604

<210> 56
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 56
Leu Ile Phe Phe Asp Ala Arg Asp Cys Cys Phe Asn Glu Gln Leu
1 5 10 15

<210> 57
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 57
Leu Glu Trp Gly Ser Asp Val Phe Tyr Asp Val Tyr Asp Cys Cys
1 5 10 15

<210> 58
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 58
Arg Ile Val Pro Asn Gly Tyr Phe Asn Val His Gly Arg Ser Leu
1 5 10 15

<210> 59
<211> 15
<212> PRT
<213> Artificial Sequence

